



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 12:20 PM UTC

PDB ID : 4H44 / pdb_00004h44
Title : 2.70 Å Cytochrome b6f Complex Structure From Nostoc PCC 7120
Authors : Hasan, S.S.; Yamashita, E.; Baniulis, D.; Cramer, W.A.
Deposited on : 2012-09-16
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

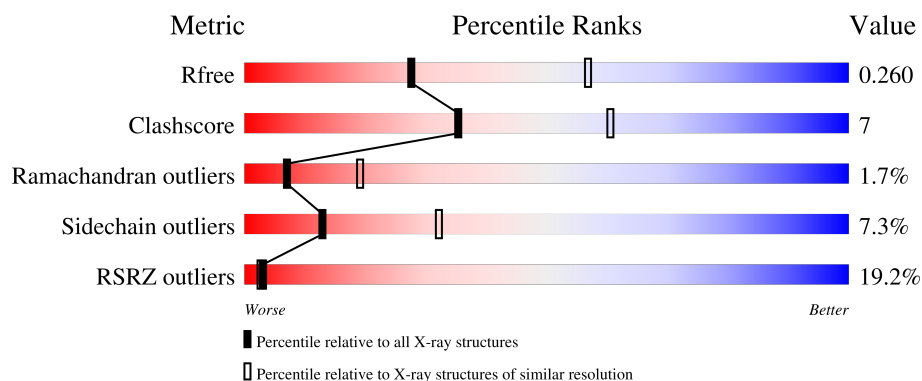
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



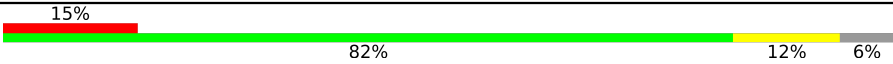
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	215	4% 80% 18% .
2	B	160	7% 78% 19% .
3	C	289	25% 79% 19% .
4	D	179	43% 82% 10% 7%
5	E	31	10% 90% 10%

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Mol	Chain	Length	Quality of chain
6	F	34	
7	G	37	
8	H	29	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	UMQ	A	304	X	-	-	-
10	UMQ	A	305	X	-	-	-
10	UMQ	A	307	X	-	-	-
10	UMQ	A	309	X	-	-	-
10	UMQ	F	101	X	-	-	-
13	CLA	B	201	X	-	-	-
16	CD	C	304	-	-	-	X

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 16386 atoms, of which 8258 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Cytochrome b6.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	215	Total	C	H	N	O	S	0	0	0
			3451	1144	1736	272	288	11			

- Molecule 2 is a protein called Cytochrome b6-f complex subunit 4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	160	Total	C	H	N	O	S	0	0	0
			2531	830	1292	195	208	6			

- Molecule 3 is a protein called Apocytochrome f.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	289	Total	C	H	N	O	S	0	0	0
			4379	1396	2184	364	429	6			

- Molecule 4 is a protein called Cytochrome b6-f complex iron-sulfur subunit 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	D	166	Total	C	H	N	O	S	0	0	0
			2459	791	1210	213	239	6			

- Molecule 5 is a protein called Cytochrome b6-f complex subunit 6.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
5	E	31	Total	C	H	N	O	S	0	0	0
			484	157	257	35	34	1			

- Molecule 6 is a protein called Cytochrome b6-f complex subunit 7.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
6	F	32	Total	C	H	N	O	S	0	0	0
			483	156	252	36	38	1			

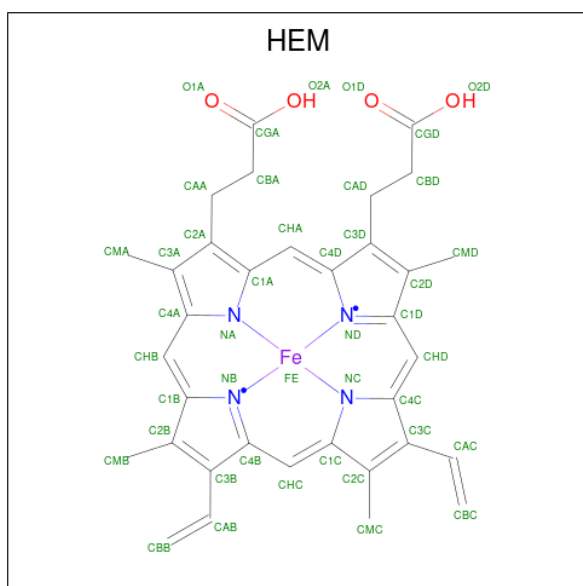
- Molecule 7 is a protein called Cytochrome b6-f complex subunit 5.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
7	G	37	Total	C	H	N	O	S	0	0	0
			584	188	303	44	48	1			

- Molecule 8 is a protein called Cytochrome b6-f complex subunit 8.

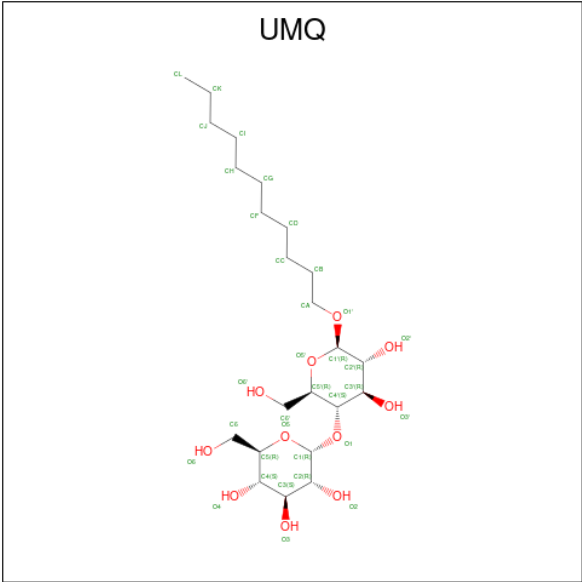
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
8	H	29	Total	C	H	N	O	S	0	0	0
			470	155	243	36	34	2			

- Molecule 9 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



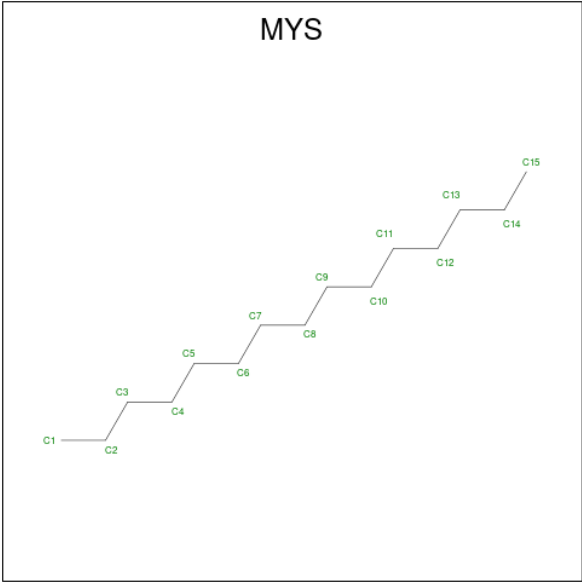
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
9	A	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
9	A	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
9	A	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
9	C	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		

- Molecule 10 is UNDECYL-MALTOSIDE (CCD ID: UMQ) (formula: $C_{23}H_{44}O_{11}$).



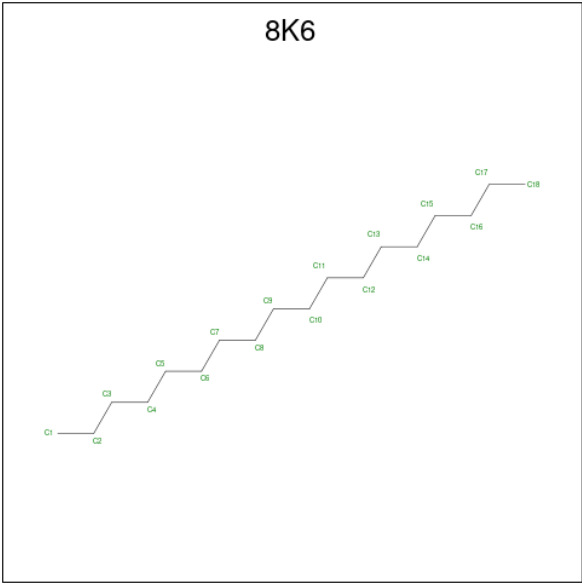
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	H	O	0	0
			77	23	43	11		
10	A	1	Total	C	H	O	0	0
			77	23	43	11		
10	A	1	Total	C	H	O	0	0
			78	23	44	11		
10	A	1	Total	C	H	O	0	0
			77	23	43	11		
10	F	1	Total	C	H	O	0	0
			77	23	43	11		

- Molecule 11 is PENTADECANE (CCD ID: MYS) (formula: C₁₅H₃₂).



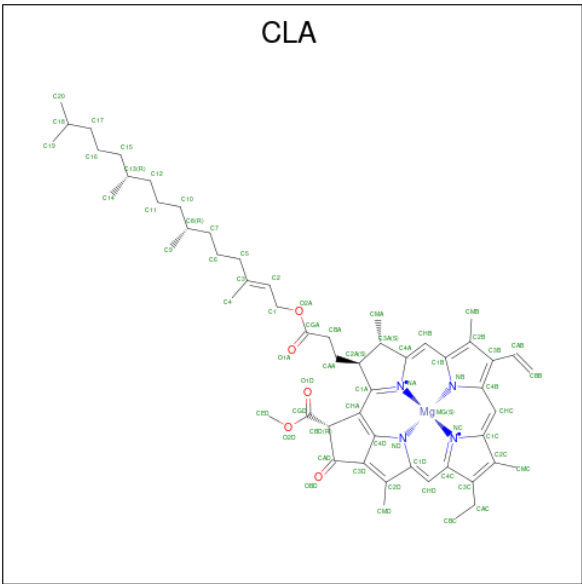
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	H	0	0
			47	15	32		

- Molecule 12 is Octadecane (CCD ID: 8K6) (formula: C₁₈H₃₈).



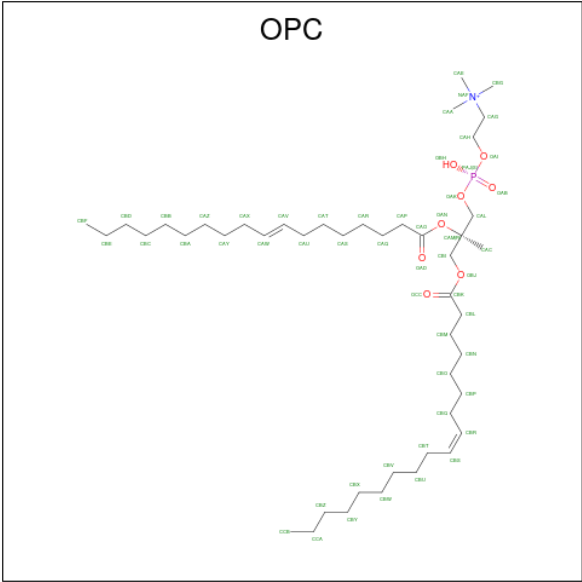
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	A	1	Total	C	H	0	0
			56	18	38		

- Molecule 13 is CHLOROPHYLL A (CCD ID: CLA) (formula: C₅₅H₇₂MgN₄O₅).



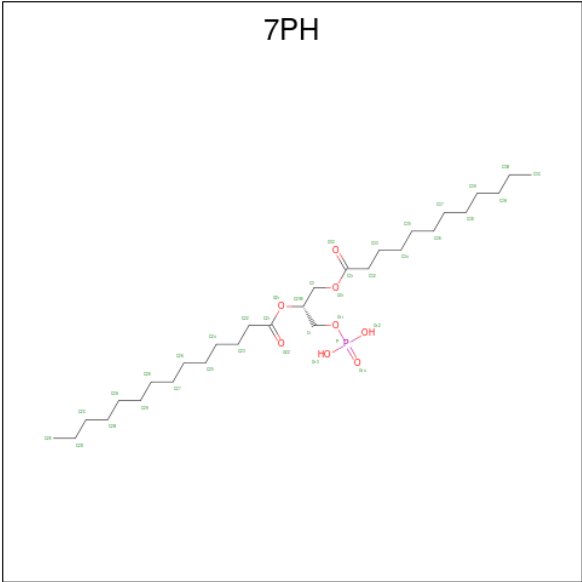
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
13	B	1	Total	C	H	Mg	N	O	0	0
			127	55	62	1	4	5		

- Molecule 14 is (7R,17E)-4-HYDROXY-N,N,N,7-TETRAMETHYL-7-[(8E)-OCTADEC-8-ENOYLOXY]-10-OXO-3,5,9-TRIOXA-4-PHOSPHAHEPTACOS-17-EN-1-AMINIUM 4-OXIDE (CCD ID: OPC) (formula: C₄₅H₈₇NO₈P).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
14	B	1	Total	C	H	N	O	P	0	0
			137	44	83	1	8	1		
14	C	1	Total	C	H	N	O	P	0	0
			137	44	83	1	8	1		

- Molecule 15 is (1R)-2-(dodecanoyloxy)-1-[(phosphonoxy)methyl]ethyl tetradecanoate (CCD ID: 7PH) (formula: C₂₉H₅₇O₈P).

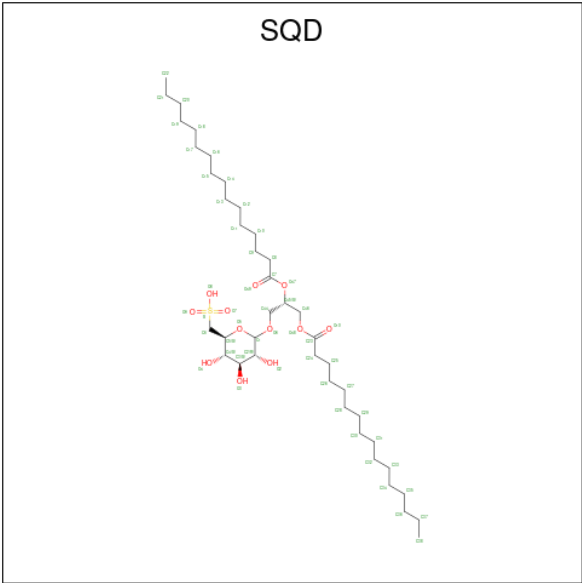


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
15	C	1	Total	C	H	O	0	0
			81	27	49	5		

- Molecule 16 is CADMIUM ION (CCD ID: CD) (formula: Cd).

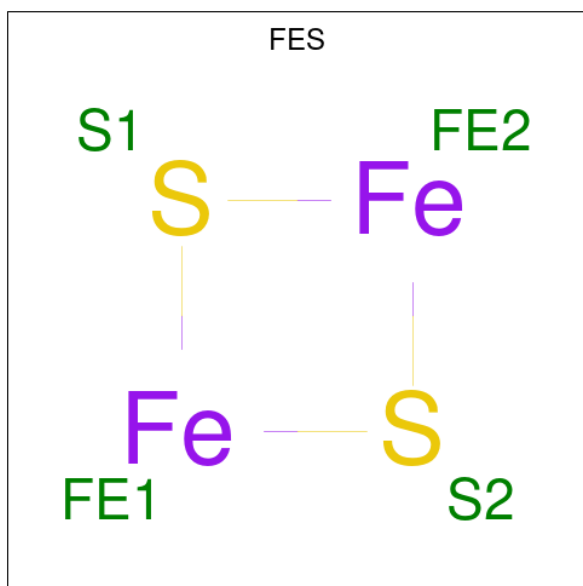
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	C	1	Total	Cd	0	0
			1	1		

- Molecule 17 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (CCD ID: SQD) (formula: C₄₁H₇₈O₁₂S).



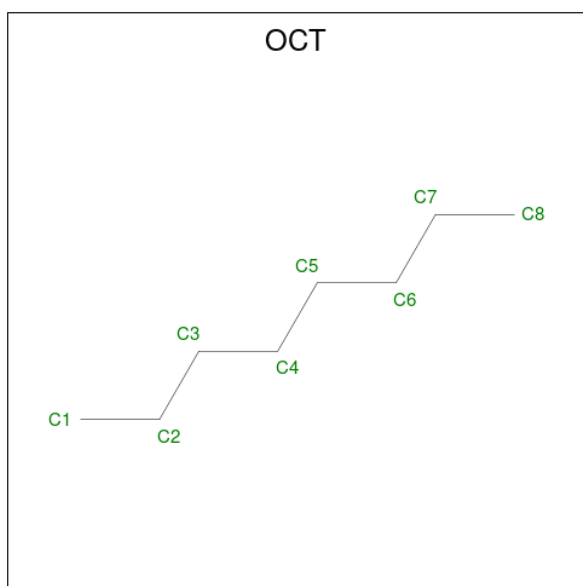
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	D	1	Total	C	H	O	S	0	0
			53	16	24	12	1		

- Molecule 18 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



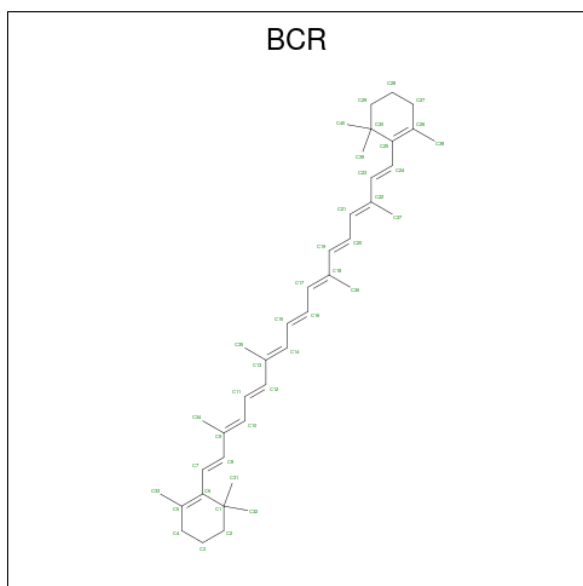
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	D	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 19 is N-OCTANE (CCD ID: OCT) (formula: C_8H_{18}).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	F	1	Total	C	H	0	0
			26	8	18		

- Molecule 20 is BETA-CAROTENE (CCD ID: BCR) (formula: $C_{40}H_{56}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
20	G	1	Total	C	H	0	0
			96	40	56		

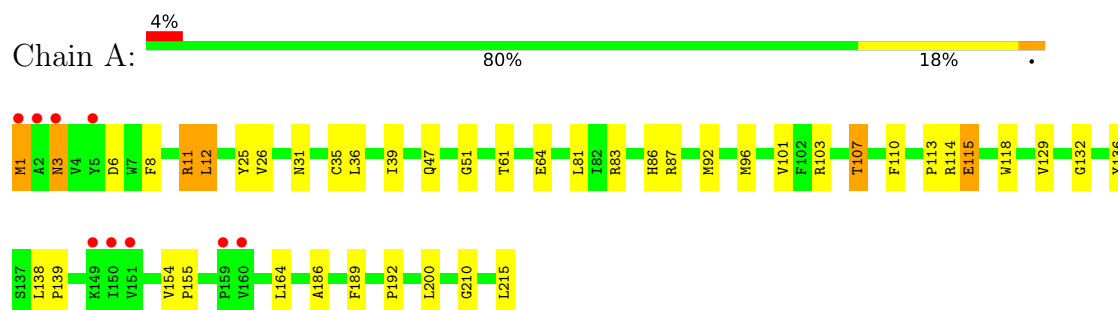
- Molecule 21 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
21	A	26	Total	O	0	0
			26	26		
21	B	22	Total	O	0	0
			22	22		
21	C	45	Total	O	0	0
			45	45		
21	D	1	Total	O	0	0
			1	1		
21	G	5	Total	O	0	0
			5	5		
21	H	3	Total	O	0	0
			3	3		

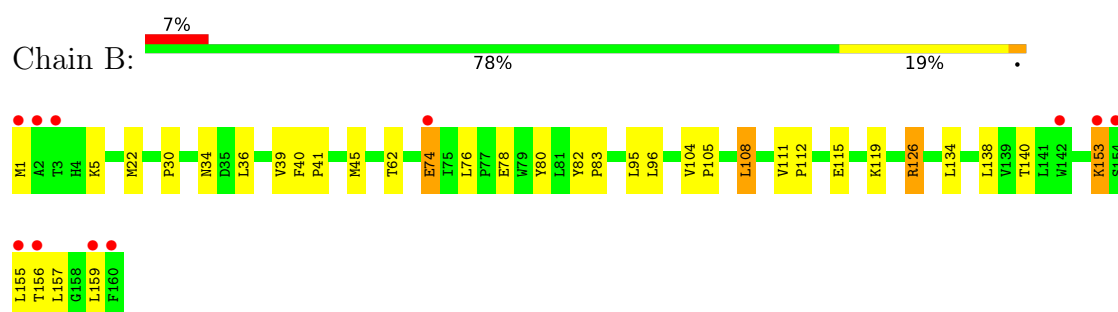
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

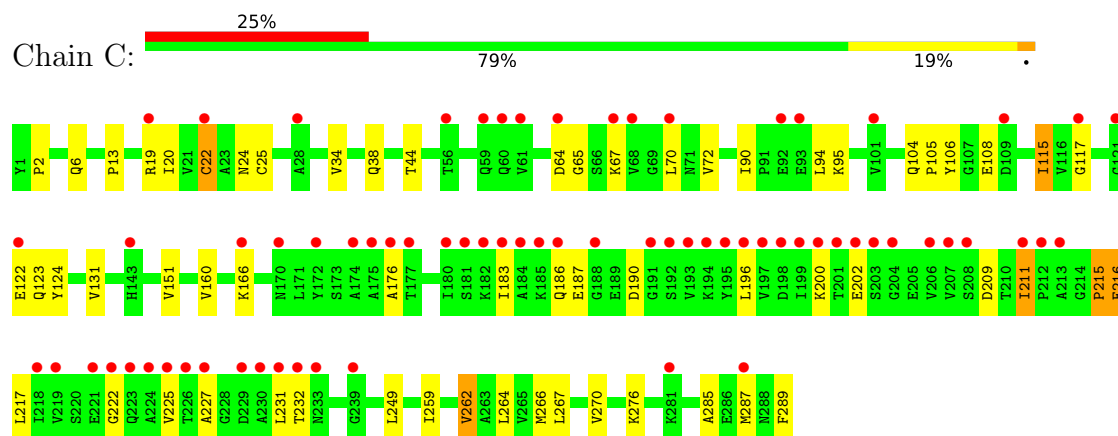
- Molecule 1: Cytochrome b6



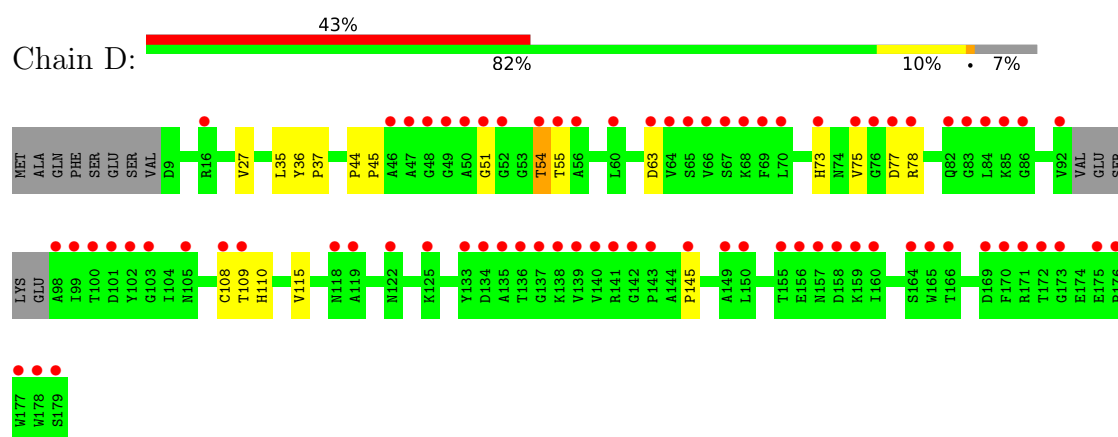
- Molecule 2: Cytochrome b6-f complex subunit 4



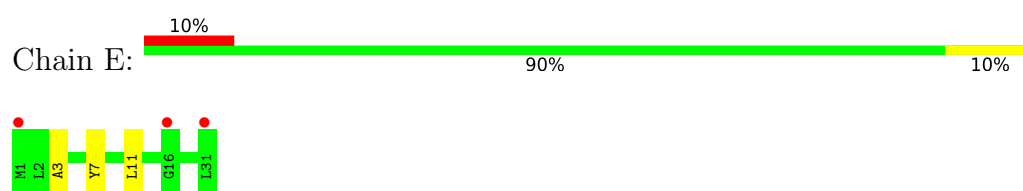
- Molecule 3: Apocytochrome f



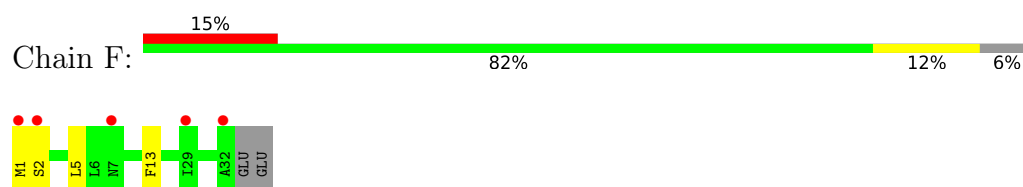
- Molecule 4: Cytochrome b6-f complex iron-sulfur subunit 1



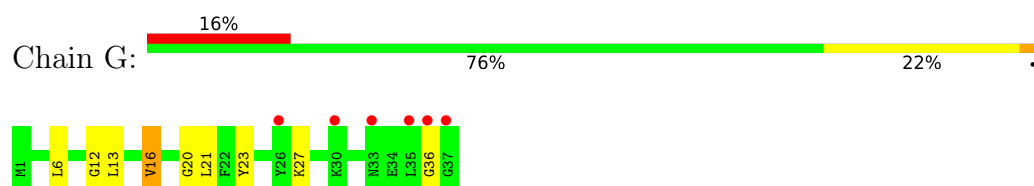
- Molecule 5: Cytochrome b6-f complex subunit 6



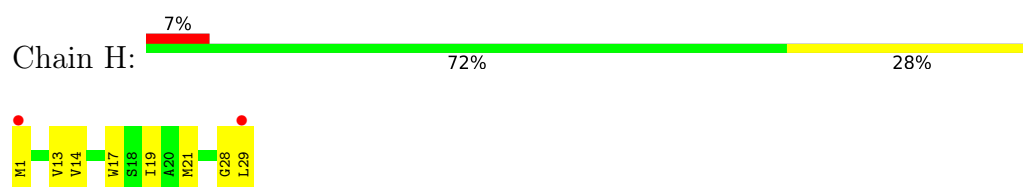
- Molecule 6: Cytochrome b6-f complex subunit 7



- Molecule 7: Cytochrome b6-f complex subunit 5



- Molecule 8: Cytochrome b6-f complex subunit 8



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	159.13Å 159.13Å 364.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.55 – 2.70 39.55 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.0 (39.55-2.70) 98.0 (39.55-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.69Å)	Xtriage
Refinement program	REFMAC, PHENIX 1.8.1_1168	Depositor
R, R_{free}	0.220 , 0.246 (Not available) , 0.260	Depositor DCC
R_{free} test set	3733 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	69.7	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 60.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	16386	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UMQ, OCT, 7PH, MYS, 8K6, CLA, HEM, OPC, FES, BCR, SQD, CD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.31	0/1768	0.70	0/2411
2	B	0.31	0/1278	0.73	2/1752 (0.1%)
3	C	0.29	0/2241	0.66	0/3053
4	D	0.28	0/1280	0.67	1/1745 (0.1%)
5	E	0.28	0/230	0.71	0/309
6	F	0.30	0/234	0.67	0/315
7	G	0.30	0/286	0.79	0/387
8	H	0.32	0/233	0.73	0/319
All	All	0.30	0/7550	0.69	3/10291 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	126	ARG	CA-C-N	5.58	125.11	119.19
2	B	126	ARG	C-N-CA	5.58	125.11	119.19
4	D	75	VAL	N-CA-C	-5.41	107.47	112.83

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1715	1736	1734	34	1
2	B	1239	1292	1290	24	0
3	C	2195	2184	2183	32	0
4	D	1249	1210	1208	9	0
5	E	227	257	257	2	0
6	F	231	252	252	4	0
7	G	281	303	303	6	0
8	H	227	243	243	11	0
9	A	129	90	90	19	0
9	C	43	30	30	7	0
10	A	136	173	166	5	0
10	F	34	43	42	1	0
11	A	15	32	32	1	0
12	A	18	38	38	0	0
13	B	65	62	72	3	0
14	B	54	83	83	0	0
14	C	54	83	83	3	0
15	C	32	49	45	0	0
16	C	1	0	0	0	0
17	D	29	24	22	0	0
18	D	4	0	0	1	0
19	F	8	18	18	0	0
20	G	40	56	56	5	0
21	A	26	0	0	5	0
21	B	22	0	0	4	0
21	C	45	0	0	3	0
21	D	1	0	0	0	0
21	G	5	0	0	0	0
21	H	3	0	0	0	0
All	All	8128	8258	8247	120	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 120 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:126:ARG:NH1	21:B:319:HOH:O	2.04	0.90
3:C:25:CYS:SG	9:C:301:HEM:CAC	2.65	0.84
1:A:35:CYS:SG	9:A:303:HEM:CAB	2.70	0.80
9:A:303:HEM:O1A	21:A:425:HOH:O	2.03	0.77
1:A:3:ASN:ND2	1:A:6:ASP:OD2	2.20	0.75

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:ARG:NH1	1:A:115:GLU:OE1[12_565]	2.04	0.16

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	213/215 (99%)	206 (97%)	6 (3%)	1 (0%)	24	48
2	B	158/160 (99%)	149 (94%)	8 (5%)	1 (1%)	21	44
3	C	287/289 (99%)	252 (88%)	27 (9%)	8 (3%)	4	9
4	D	162/179 (90%)	136 (84%)	22 (14%)	4 (2%)	4	11
5	E	29/31 (94%)	28 (97%)	1 (3%)	0	100	100
6	F	30/34 (88%)	28 (93%)	1 (3%)	1 (3%)	3	7
7	G	35/37 (95%)	34 (97%)	0	1 (3%)	3	9
8	H	27/29 (93%)	27 (100%)	0	0	100	100
All	All	941/974 (97%)	860 (91%)	65 (7%)	16 (2%)	7	19

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	190	ASP
3	C	216	GLU
4	D	78	ARG
3	C	200	LYS
3	C	222	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	184/184 (100%)	171 (93%)	13 (7%)	13	33
2	B	134/134 (100%)	120 (90%)	14 (10%)	7	17
3	C	238/238 (100%)	217 (91%)	21 (9%)	9	23
4	D	133/145 (92%)	128 (96%)	5 (4%)	29	58
5	E	21/21 (100%)	21 (100%)	0	100	100
6	F	22/24 (92%)	22 (100%)	0	100	100
7	G	29/29 (100%)	25 (86%)	4 (14%)	3	9
8	H	24/24 (100%)	24 (100%)	0	100	100
All	All	785/799 (98%)	728 (93%)	57 (7%)	13	32

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	22	CYS
7	G	21	LEU
3	C	122	GLU
7	G	16	VAL
4	D	54	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	138	ASN
3	C	143	HIS
6	F	7	ASN
4	D	74	ASN
3	C	123	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 1 is monoatomic - leaving 19 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
18	FES	D	202	4	0,4,4	-	-	-		
15	7PH	C	303	-	31,31,37	1.00	2 (6%)	33,33,42	1.20	3 (9%)
10	UMQ	A	307	-	35,35,35	1.28	5 (14%)	46,46,46	2.02	11 (23%)
14	OPC	C	302	-	53,53,54	1.01	4 (7%)	59,61,64	0.99	2 (3%)
10	UMQ	F	101	-	35,35,35	1.31	6 (17%)	46,46,46	2.03	13 (28%)
10	UMQ	A	305	-	35,35,35	1.35	6 (17%)	46,46,46	2.11	8 (17%)
17	SQD	D	201	-	27,29,54	1.87	8 (29%)	37,40,65	4.81	9 (24%)
11	MYS	A	306	-	14,14,14	0.38	0	13,13,13	0.81	0
9	HEM	A	302	1	50,50,50	1.88	9 (18%)	67,82,82	1.23	3 (4%)
12	8K6	A	308	-	17,17,17	0.24	0	16,16,16	0.57	0
9	HEM	A	303	-	50,50,50	2.01	9 (18%)	67,82,82	1.42	6 (8%)
10	UMQ	A	309	-	35,35,35	1.27	5 (14%)	46,46,46	2.04	12 (26%)
9	HEM	C	301	3	50,50,50	1.82	8 (16%)	67,82,82	1.22	3 (4%)
13	CLA	B	201	21	69,73,73	1.19	6 (8%)	82,113,113	1.21	6 (7%)
19	OCT	F	102	-	7,7,7	0.33	0	6,6,6	0.70	0
14	OPC	B	202	-	53,53,54	0.99	4 (7%)	59,61,64	1.01	1 (1%)
9	HEM	A	301	1	50,50,50	2.01	7 (14%)	67,82,82	1.36	5 (7%)
20	BCR	G	101	-	41,41,41	2.16	20 (48%)	56,56,56	2.20	19 (33%)
10	UMQ	A	304	-	35,35,35	1.28	6 (17%)	46,46,46	2.06	10 (21%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	FES	D	202	4	-	-	0/1/1/1
15	7PH	C	303	-	-	13/33/33/39	-
10	UMQ	A	307	-	2/2/10/10	13/20/60/60	0/2/2/2
14	OPC	C	302	-	-	28/57/57/60	-
10	UMQ	F	101	-	2/2/10/10	6/20/60/60	0/2/2/2
10	UMQ	A	305	-	2/2/10/10	5/20/60/60	0/2/2/2
17	SQD	D	201	-	-	6/23/43/69	0/1/1/1
11	MYS	A	306	-	-	3/12/12/12	-
9	HEM	A	302	1	-	1/14/54/54	-
12	8K6	A	308	-	-	7/15/15/15	-
9	HEM	A	303	-	-	4/14/54/54	-
10	UMQ	A	309	-	2/2/10/10	12/20/60/60	0/2/2/2
9	HEM	C	301	3	-	3/14/54/54	-
13	CLA	B	201	21	1/1/17/20	8/39/115/115	-
19	OCT	F	102	-	-	0/5/5/5	-
14	OPC	B	202	-	-	25/57/57/60	-
9	HEM	A	301	1	-	3/14/54/54	-
20	BCR	G	101	-	-	19/29/63/63	0/2/2/2
10	UMQ	A	304	-	2/2/10/10	12/20/60/60	0/2/2/2

The worst 5 of 105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	301	HEM	C3D-C2D	8.03	1.54	1.36
9	A	303	HEM	C3D-C2D	7.91	1.53	1.36
9	A	301	HEM	C3D-C2D	7.90	1.53	1.36
9	A	302	HEM	C3D-C2D	7.66	1.53	1.36
9	A	301	HEM	FE-ND	6.89	2.16	1.94

The worst 5 of 111 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	D	201	SQD	O7-S-C6	20.20	136.92	106.76
17	D	201	SQD	O9-S-C6	-16.23	82.53	106.76
17	D	201	SQD	O9-S-O7	-9.75	82.10	113.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	305	UMQ	O1'-C1'-C2'	7.44	119.57	108.27
10	F	101	UMQ	O5-C5-C4	6.36	121.17	109.70

5 of 11 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
10	A	304	UMQ	C5'
10	A	304	UMQ	C2'
10	A	305	UMQ	C5'
10	A	305	UMQ	C1'
10	A	307	UMQ	C3'

5 of 168 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	307	UMQ	O5'-C1'-O1'-CA
10	F	101	UMQ	O5'-C1'-O1'-CA
13	B	201	CLA	C1A-C2A-CAA-CBA
13	B	201	CLA	C3A-C2A-CAA-CBA
14	B	202	OPC	CAL-OAK-PAJ-OAB

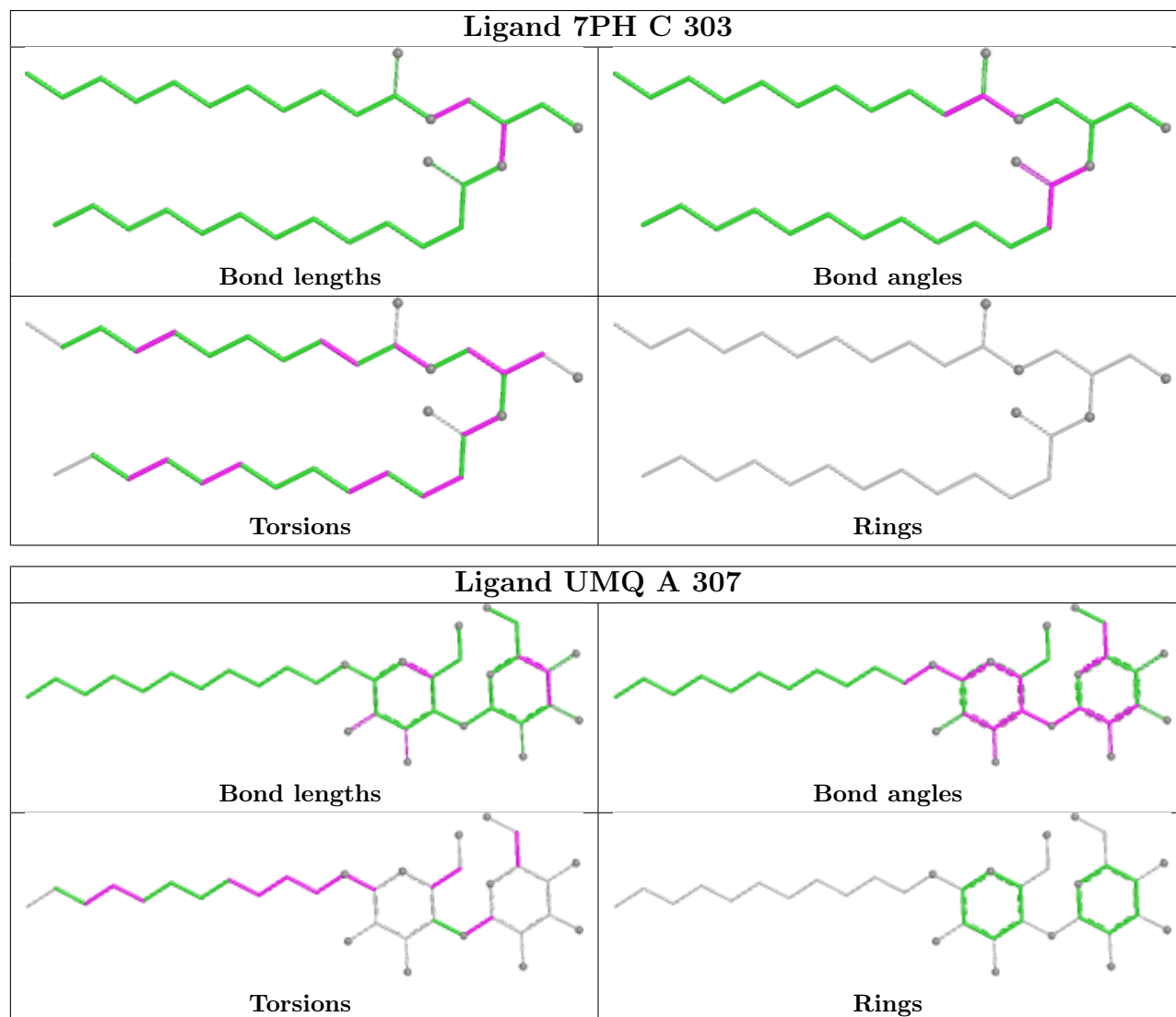
There are no ring outliers.

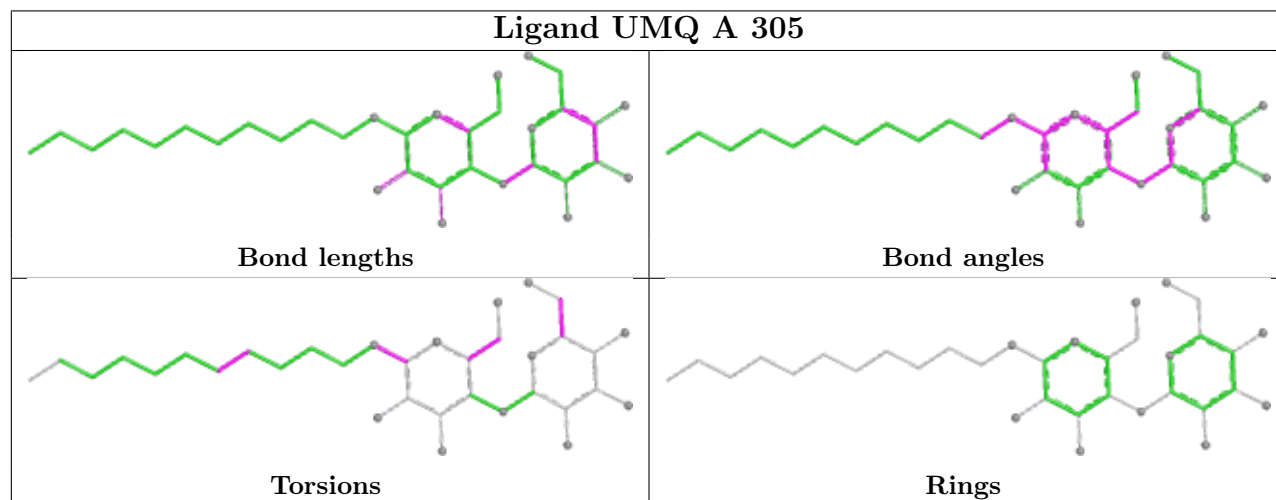
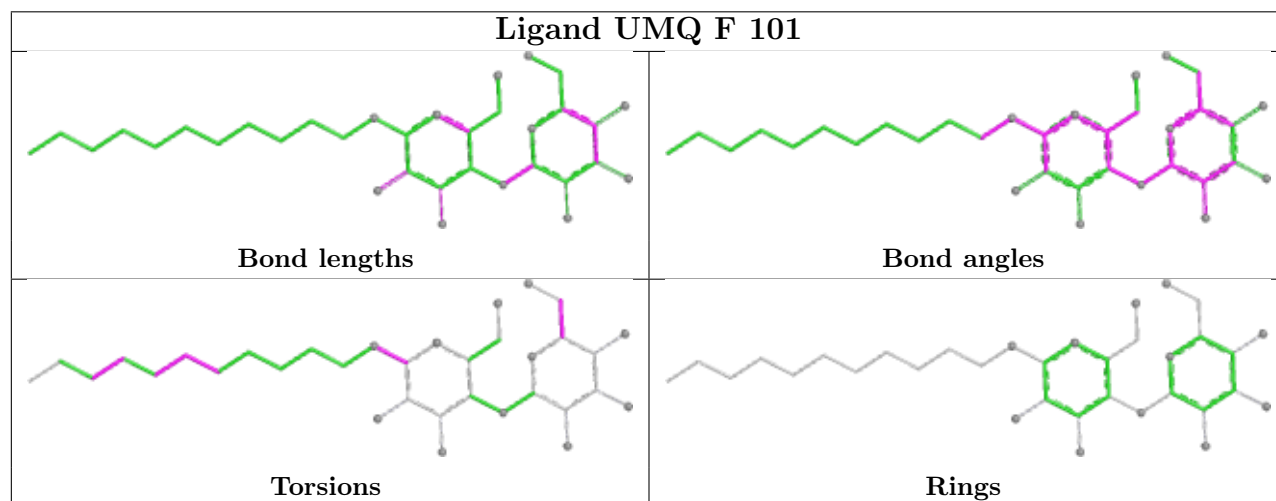
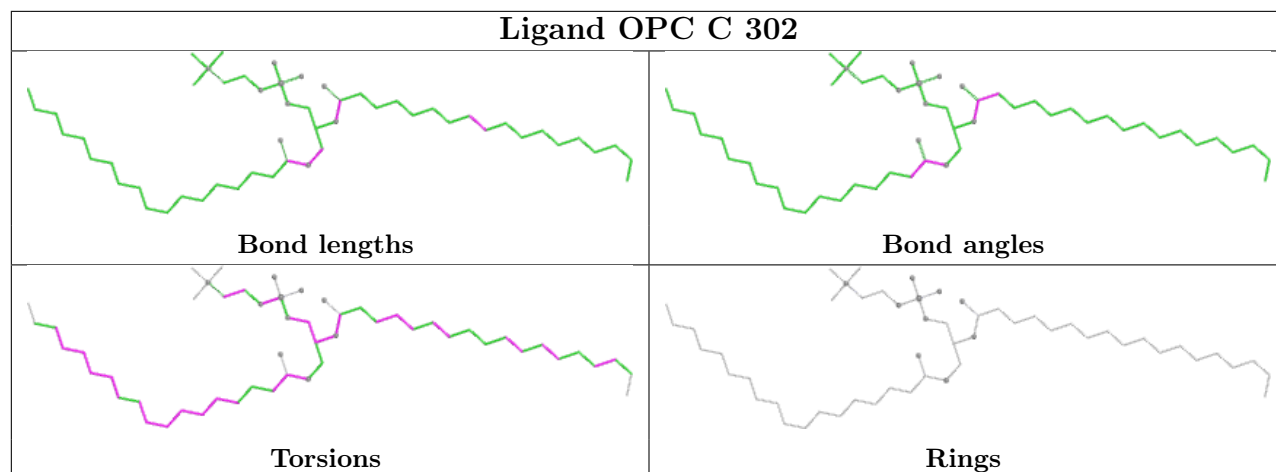
11 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	D	202	FES	1	0
10	A	307	UMQ	5	0
14	C	302	OPC	3	0
10	F	101	UMQ	1	0
11	A	306	MYS	1	0
9	A	302	HEM	4	0
9	A	303	HEM	10	0
9	C	301	HEM	7	0
13	B	201	CLA	3	0
9	A	301	HEM	5	0
20	G	101	BCR	5	0

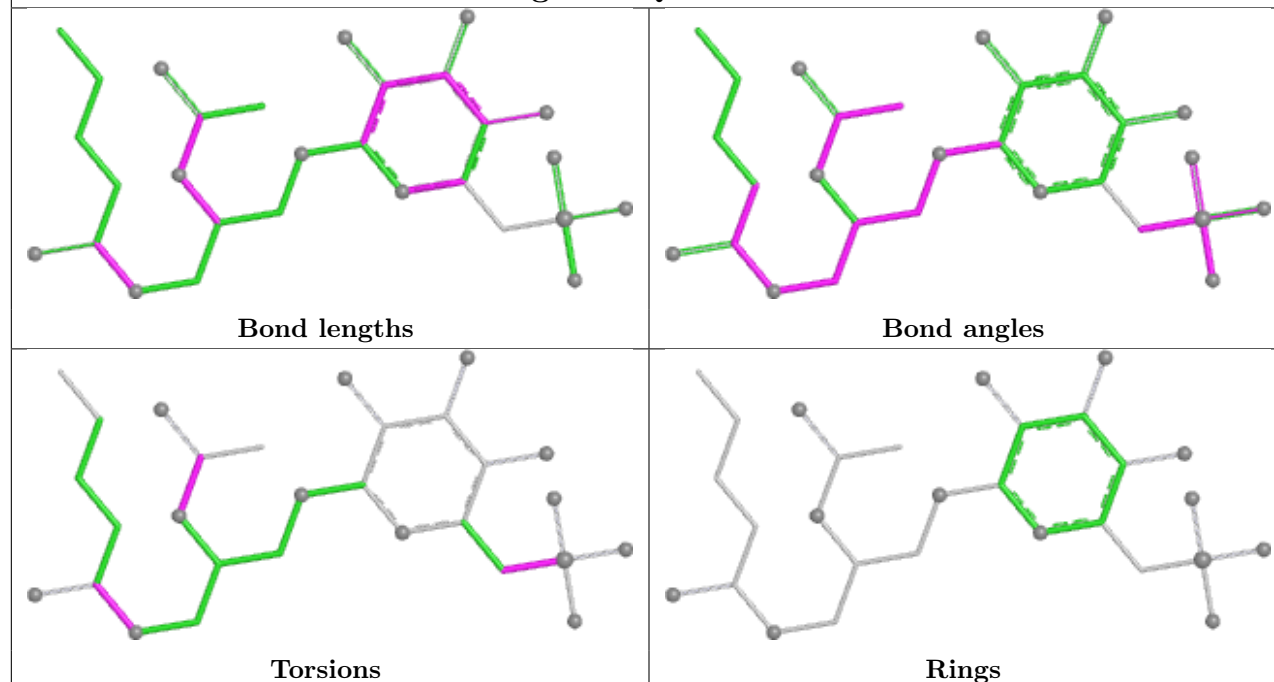
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

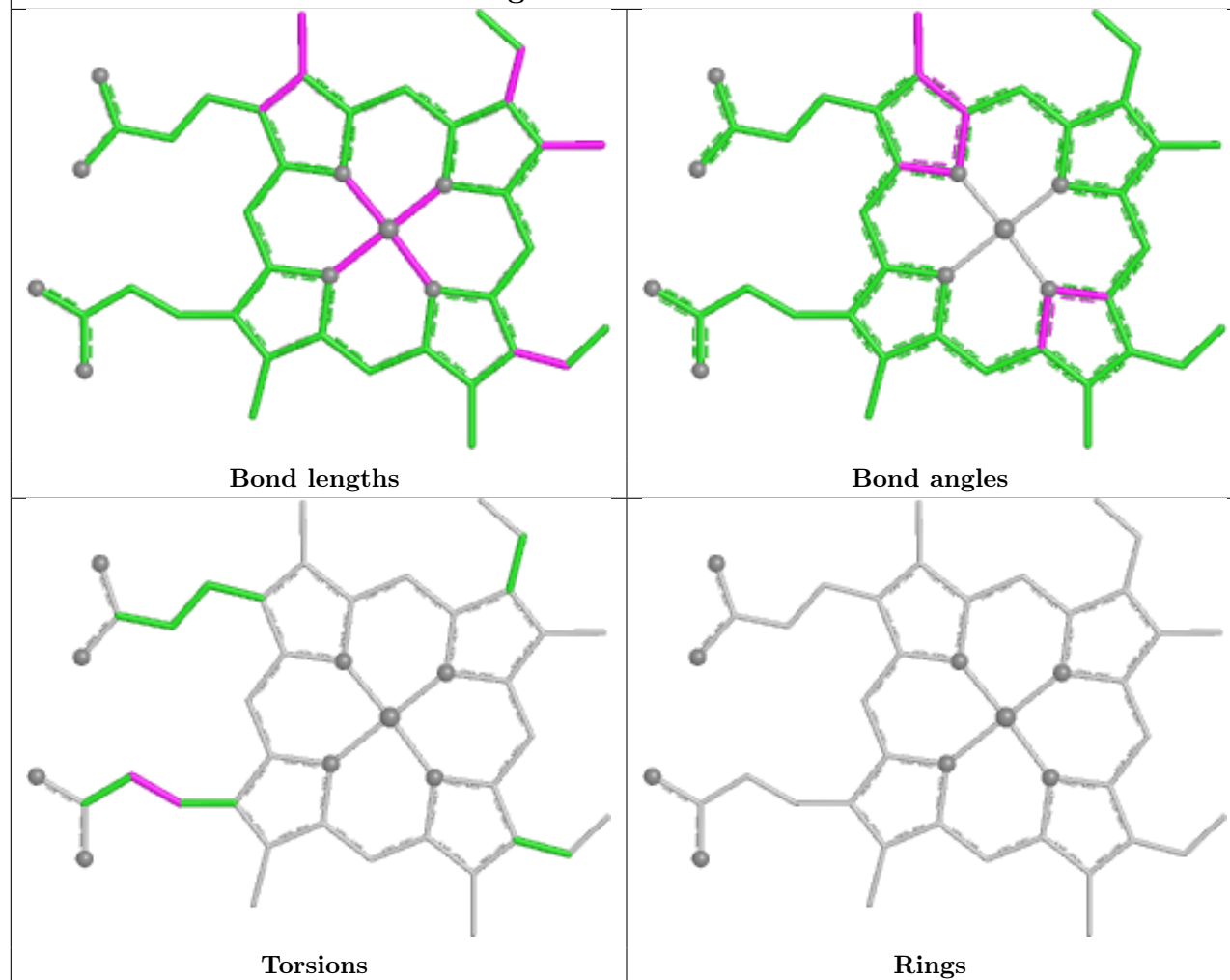


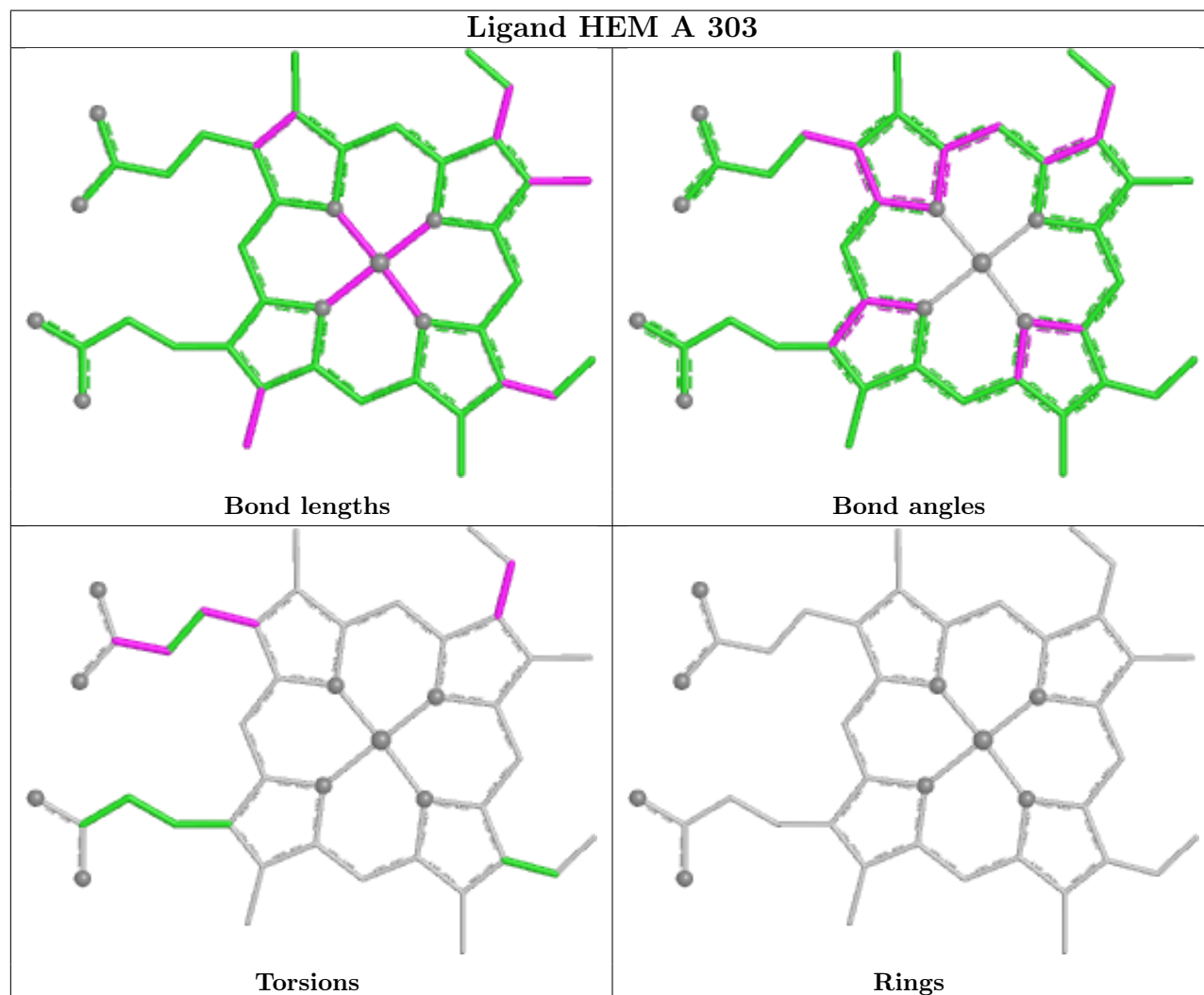
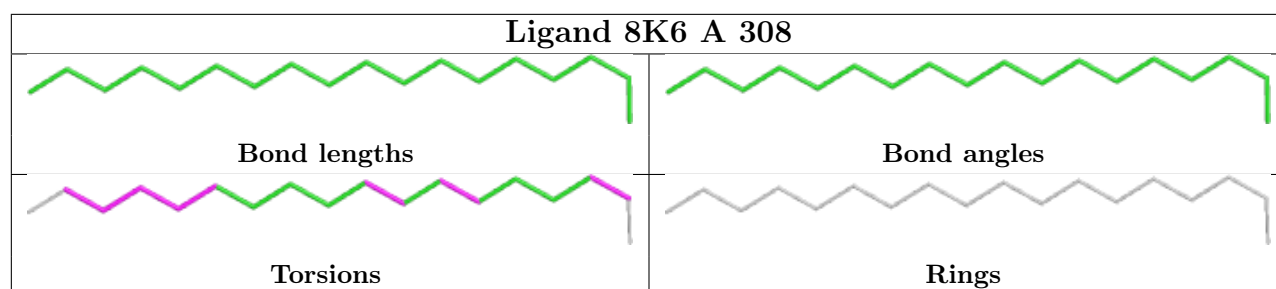


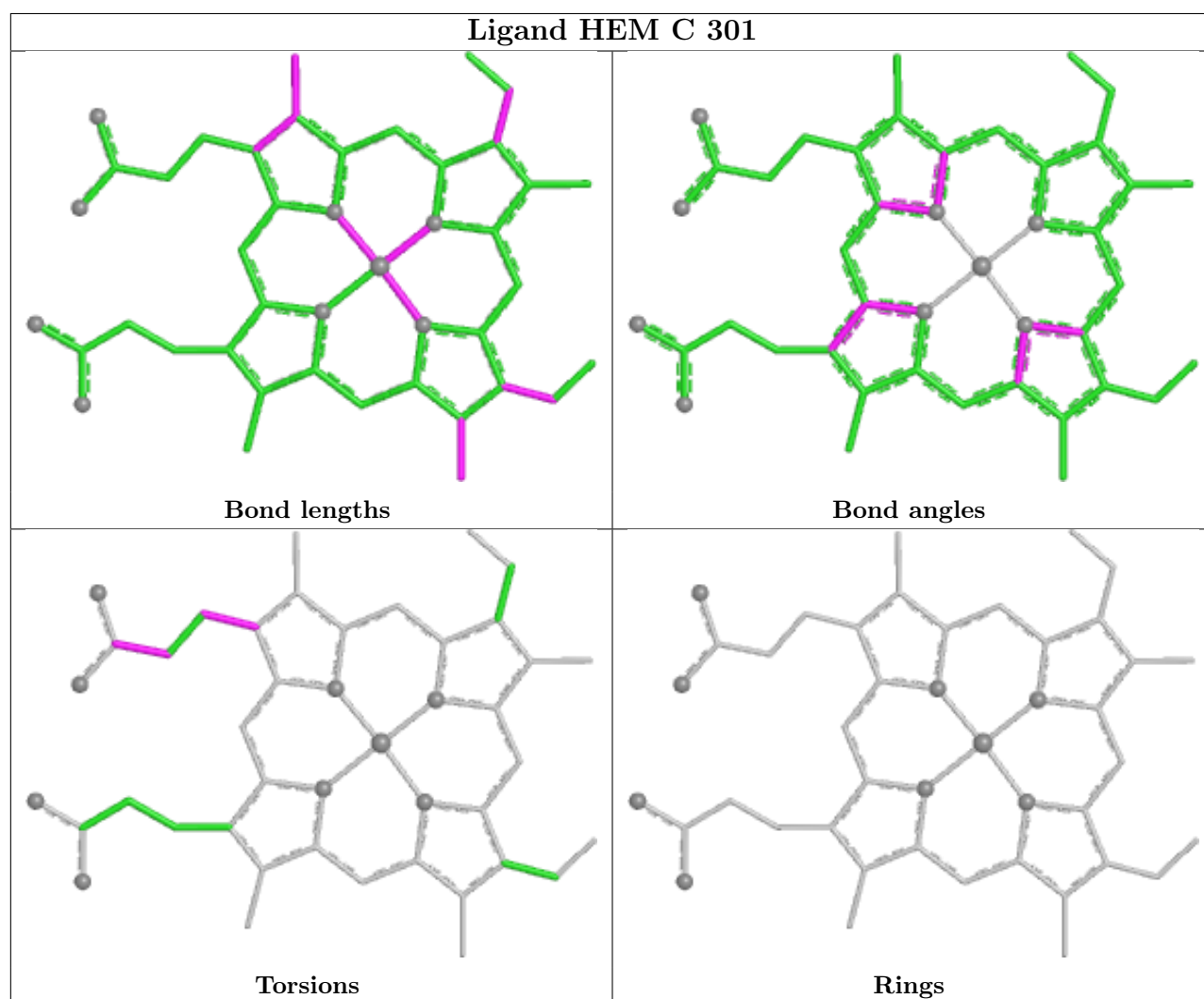
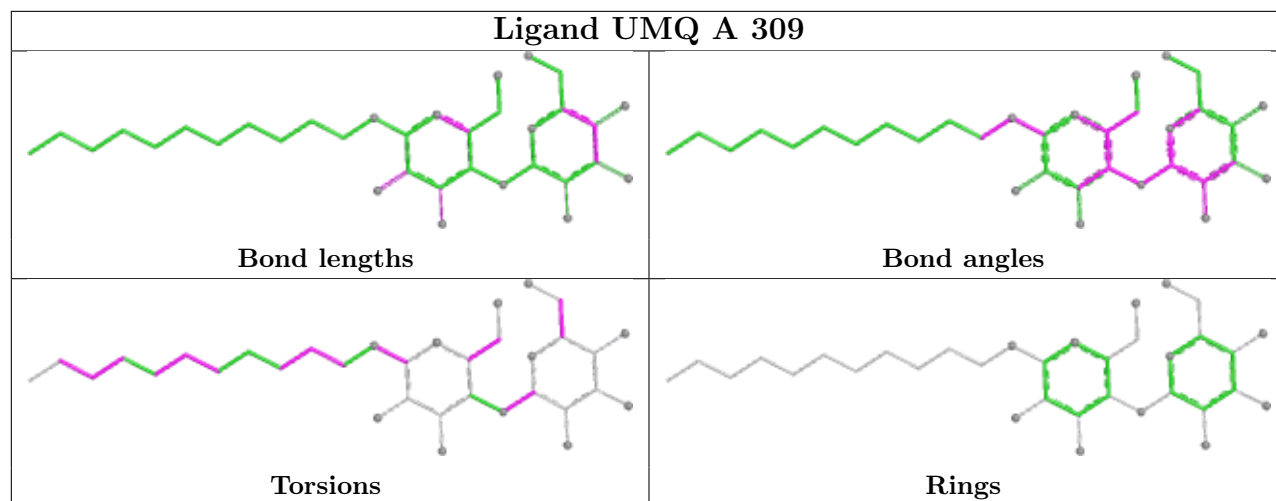
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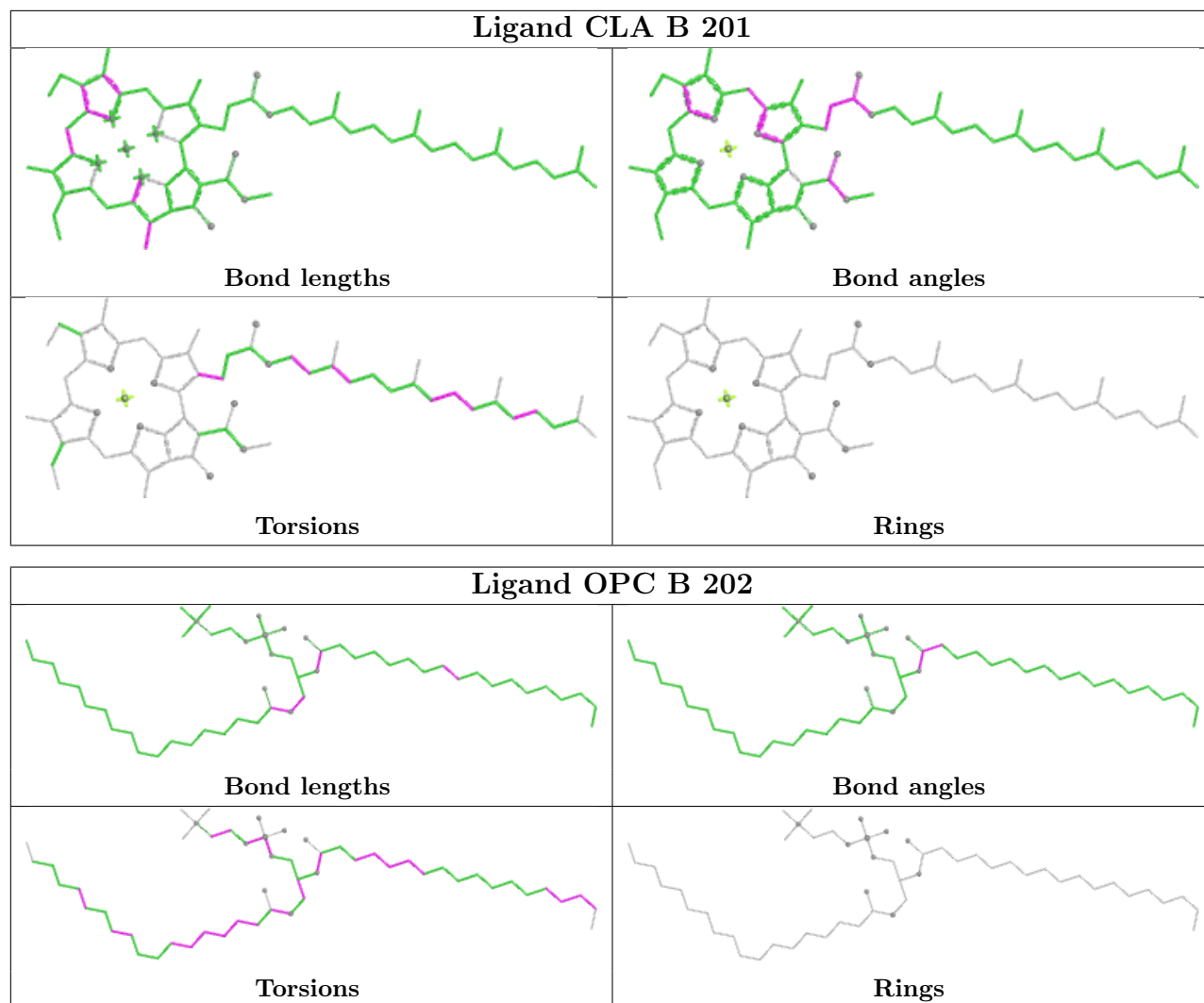


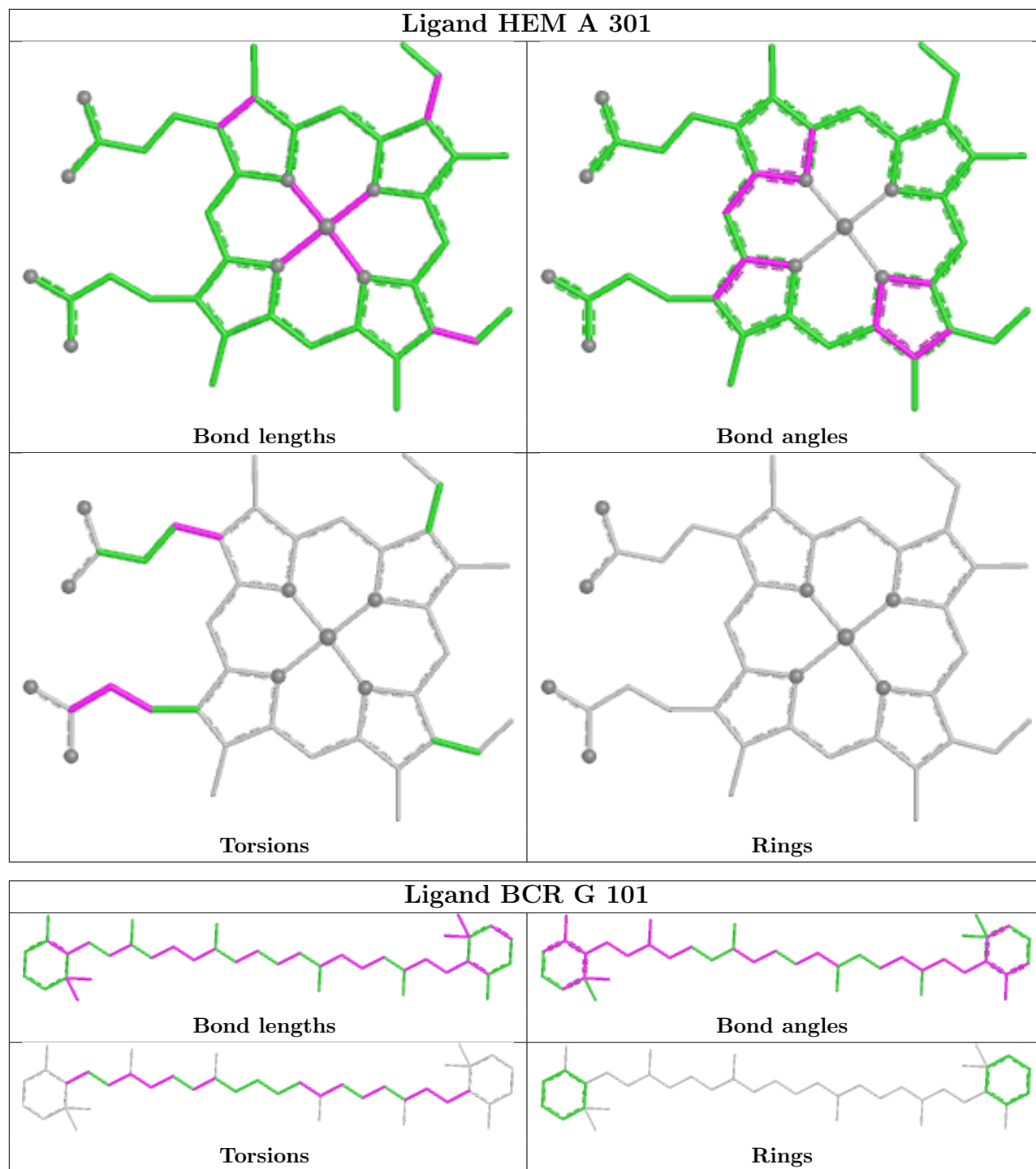
Ligand HEM A 302

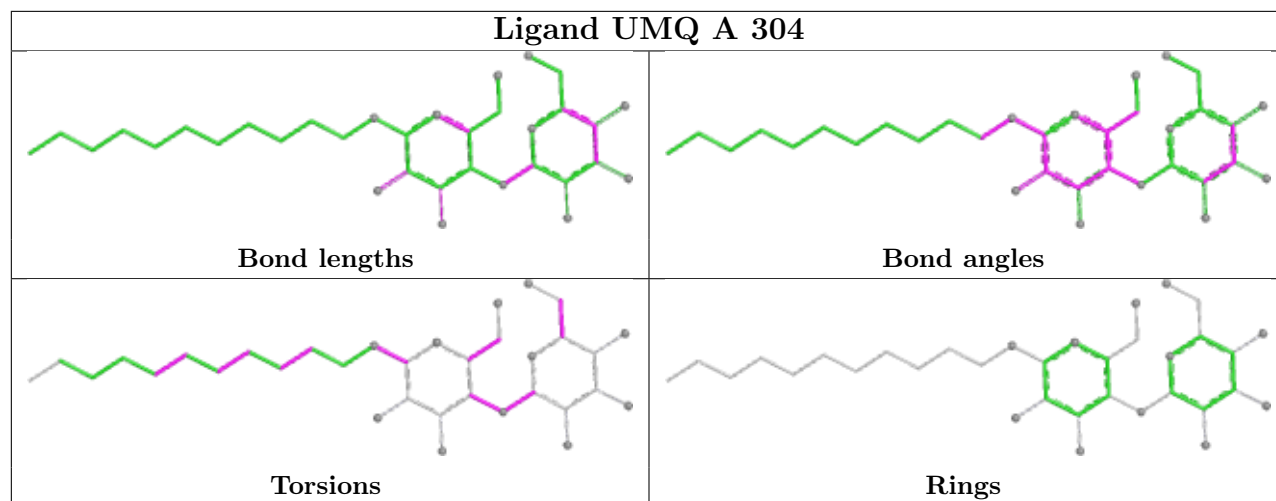












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	215/215 (100%)	-0.08	9 (4%) 40 37	31, 47, 82, 181	0
2	B	160/160 (100%)	0.47	11 (6%) 23 20	43, 64, 111, 138	0
3	C	289/289 (100%)	1.20	71 (24%) 2 1	44, 73, 182, 204	0
4	D	166/179 (92%)	2.02	77 (46%) 0 0	38, 131, 181, 193	0
5	E	31/31 (100%)	0.82	3 (9%) 13 11	66, 81, 112, 130	0
6	F	32/34 (94%)	0.88	5 (15%) 5 4	57, 72, 116, 137	0
7	G	37/37 (100%)	1.10	6 (16%) 4 4	48, 61, 115, 126	0
8	H	29/29 (100%)	0.35	2 (6%) 23 20	51, 62, 71, 101	0
All	All	959/974 (98%)	0.88	184 (19%) 3 3	31, 68, 174, 204	0

The worst 5 of 184 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	98	ALA	11.0
7	G	37	GLY	11.0
4	D	50	ALA	9.0
4	D	70	LEU	7.8
4	D	75	VAL	6.6

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

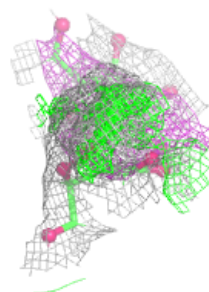
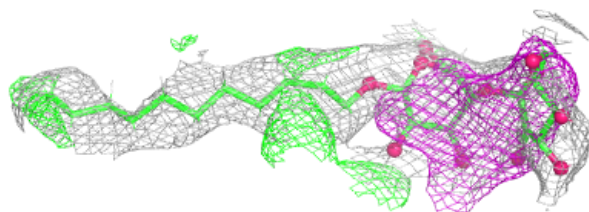
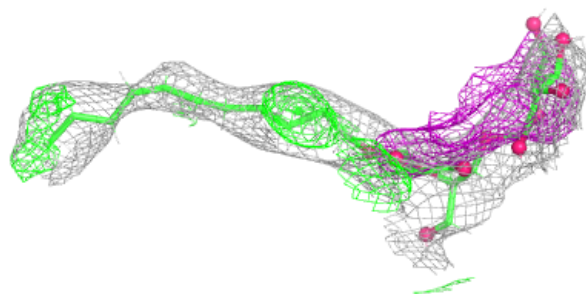
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
16	CD	C	304	1/1	0.06	0.48	206,206,206,206	0
10	UMQ	A	307	34/34	0.66	0.27	72,111,140,165	0
10	UMQ	A	304	34/34	0.66	0.25	78,129,162,173	0
10	UMQ	A	309	34/34	0.71	0.21	57,121,187,208	0
10	UMQ	F	101	34/34	0.78	0.21	63,128,205,215	0
19	OCT	F	102	8/8	0.78	0.21	61,76,90,99	0
10	UMQ	A	305	34/34	0.83	0.17	58,110,148,166	0
11	MYS	A	306	15/15	0.85	0.20	50,68,96,98	0
15	7PH	C	303	32/38	0.85	0.18	49,72,135,154	0
17	SQD	D	201	29/54	0.87	0.18	63,90,129,145	0
14	OPC	C	302	54/55	0.87	0.22	47,96,152,167	0
14	OPC	B	202	54/55	0.89	0.21	52,93,137,149	0
12	8K6	A	308	18/18	0.91	0.12	50,71,84,87	0
20	BCR	G	101	40/40	0.91	0.17	40,73,127,138	0
13	CLA	B	201	65/65	0.92	0.14	47,73,127,132	0
18	FES	D	202	4/4	0.95	0.09	79,81,82,95	0
9	HEM	A	303	43/43	0.97	0.09	40,60,72,79	0
9	HEM	C	301	43/43	0.97	0.13	34,61,83,89	0
9	HEM	A	301	43/43	0.98	0.09	29,39,55,66	0
9	HEM	A	302	43/43	0.98	0.09	23,42,53,56	0

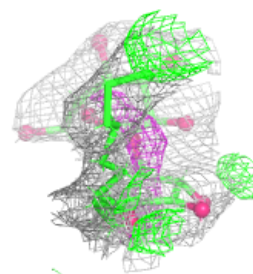
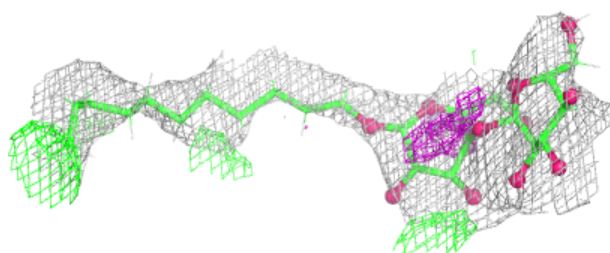
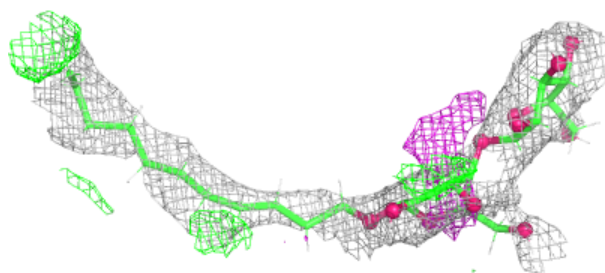
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around UMQ A 307:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

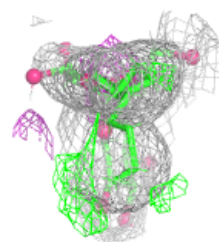
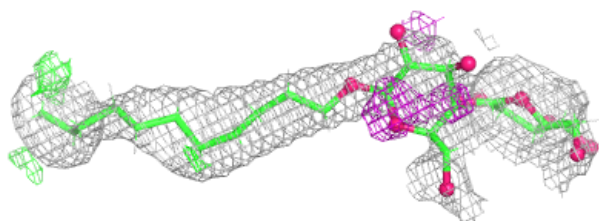
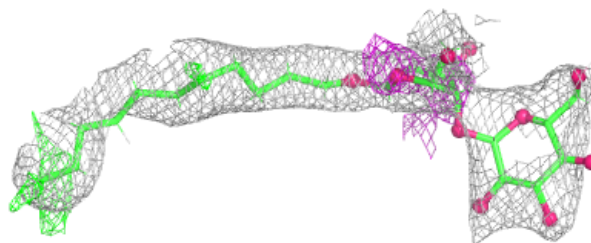
**Electron density around UMQ A 304:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

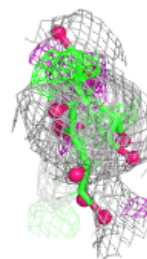
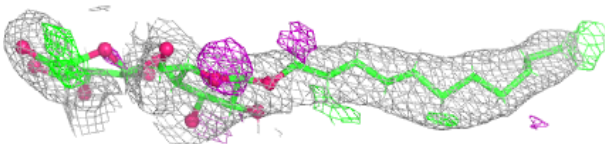
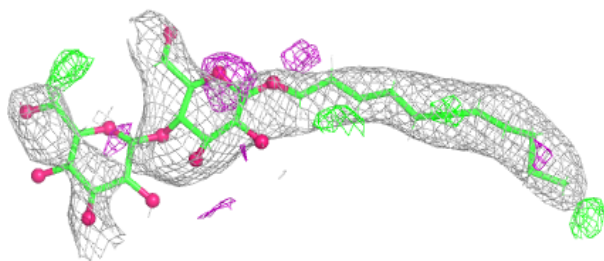


Electron density around UMQ A 309:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

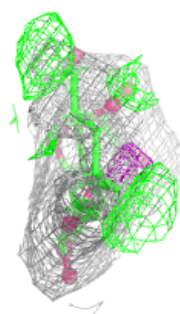
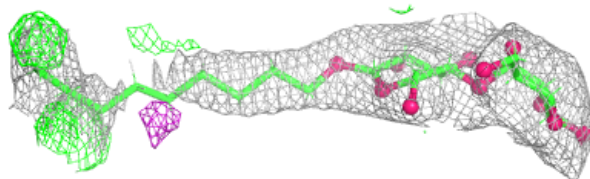
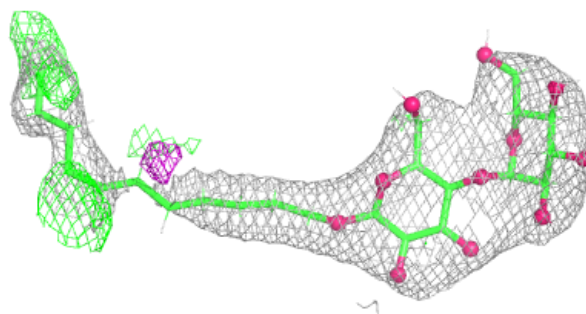
**Electron density around UMQ F 101:**

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and green (positive)

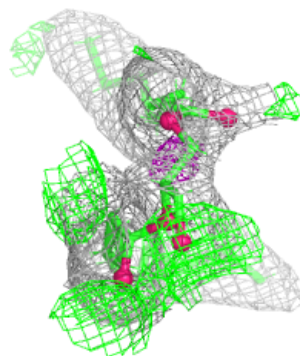
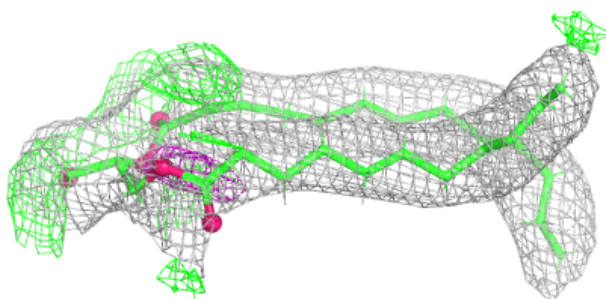
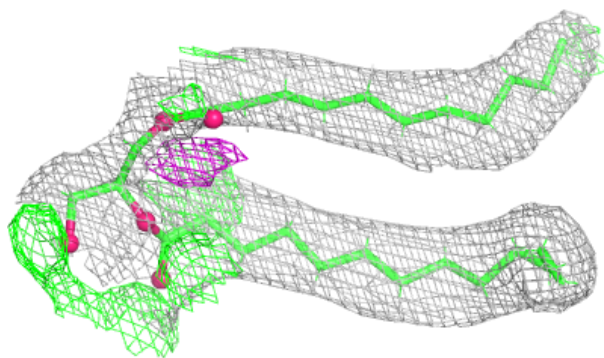


Electron density around UMQ A 305:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

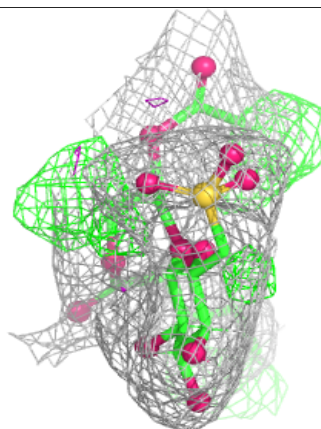
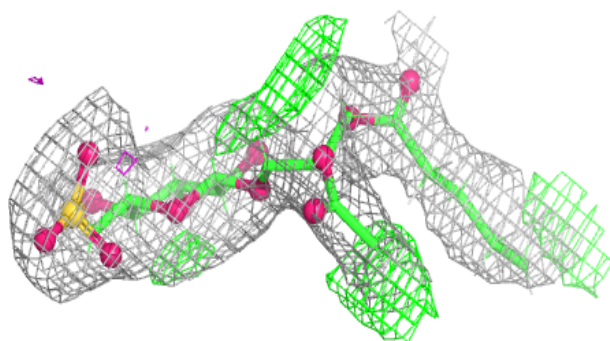
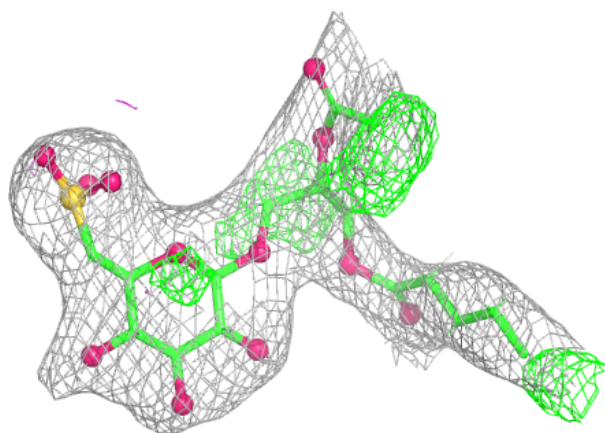
**Electron density around 7PH C 303:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



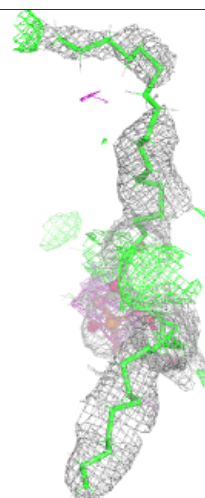
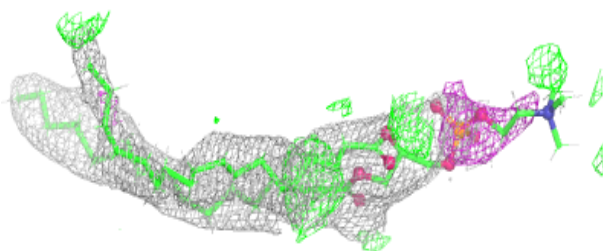
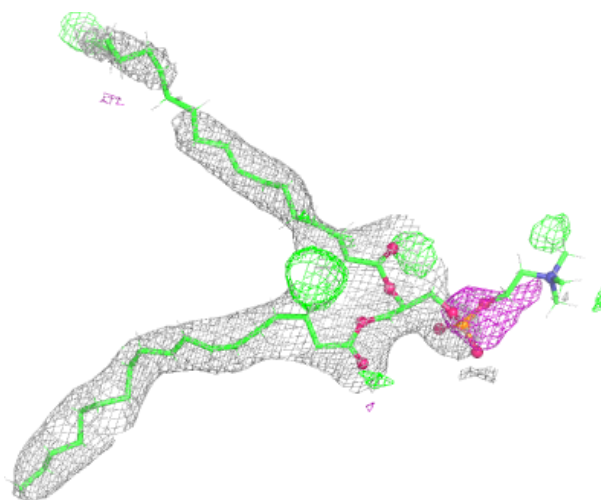
Electron density around SQD D 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



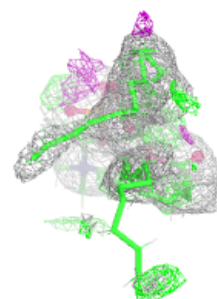
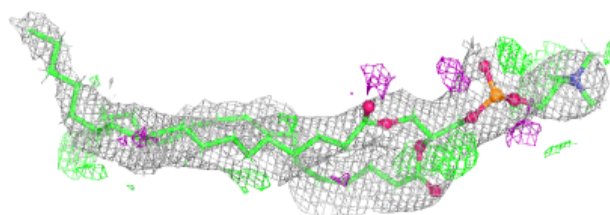
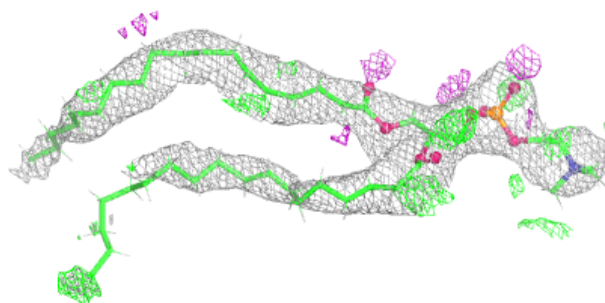
Electron density around OPC C 302:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

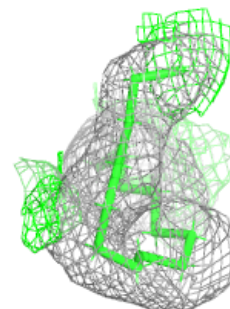
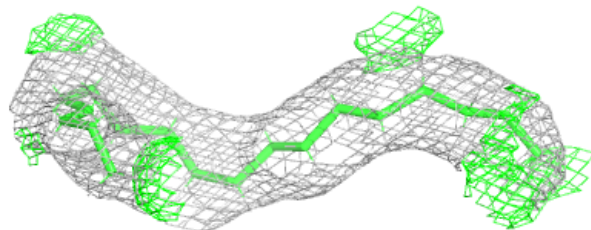
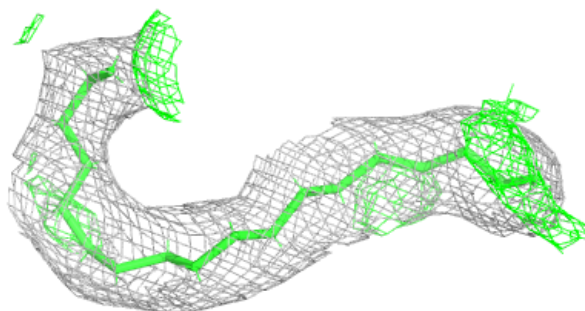


Electron density around OPC B 202:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

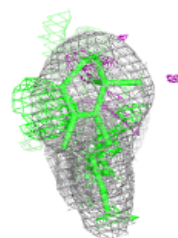
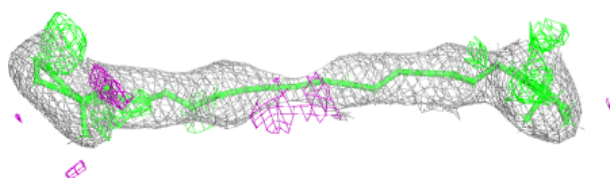
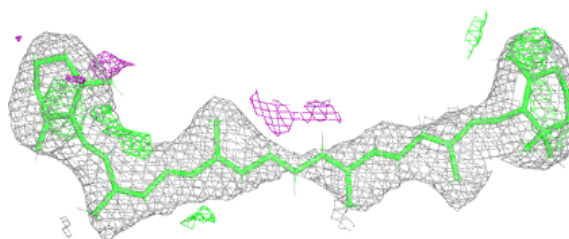
**Electron density around 8K6 A 308:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

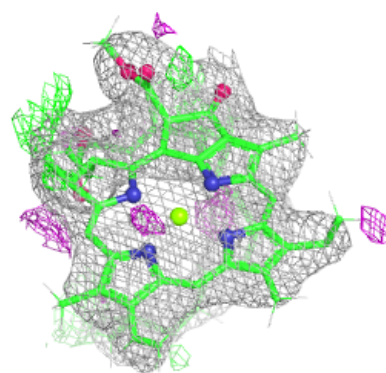
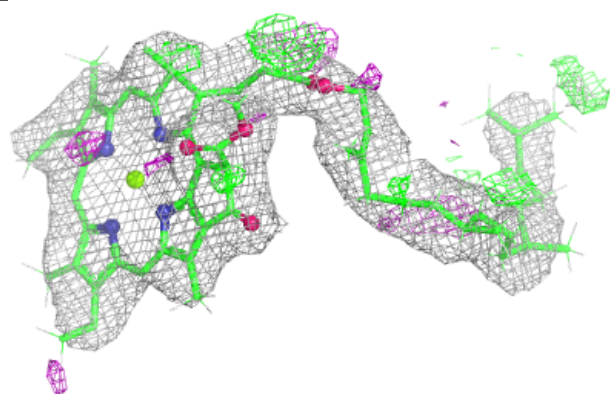
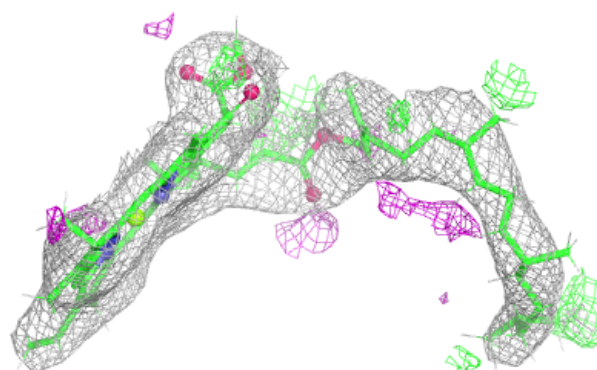


Electron density around BCR G 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

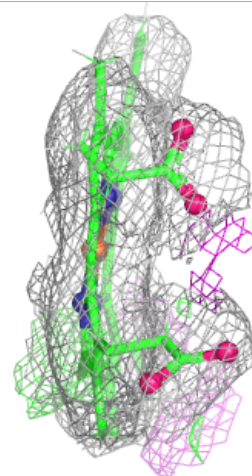
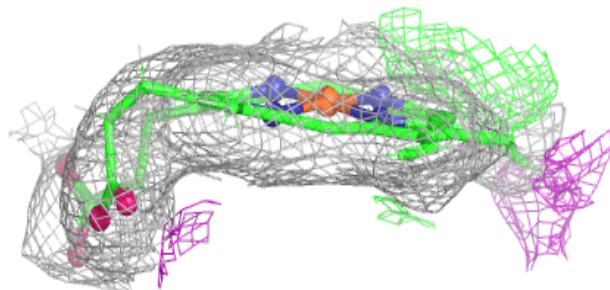
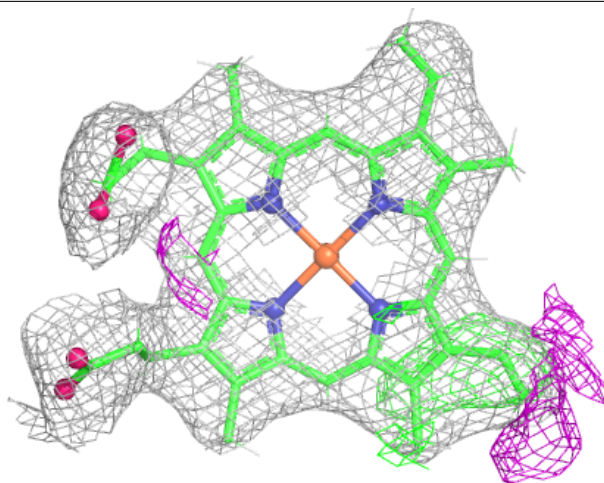
**Electron density around CLA B 201:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



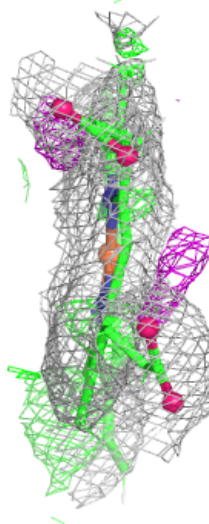
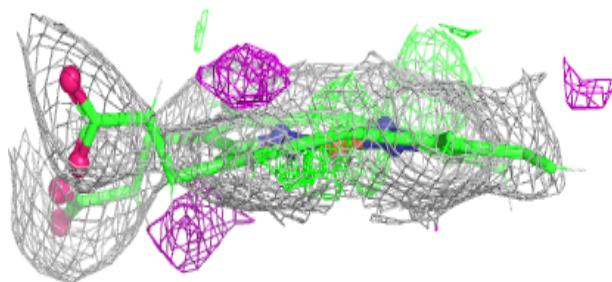
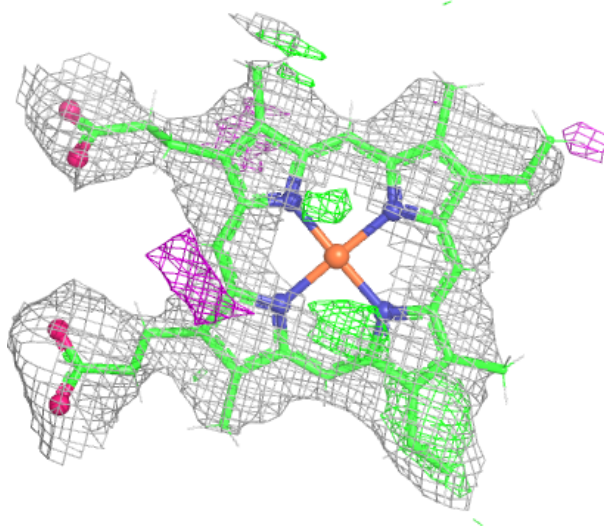
Electron density around HEM A 303:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



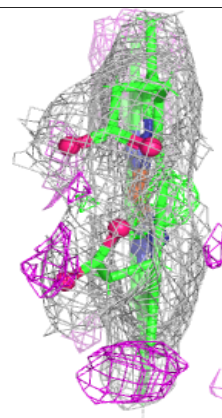
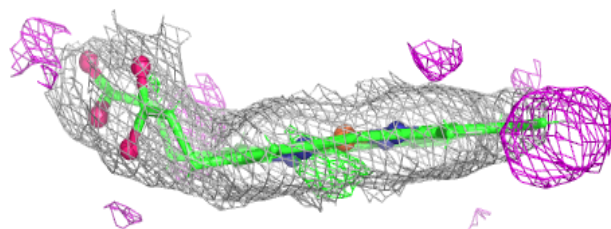
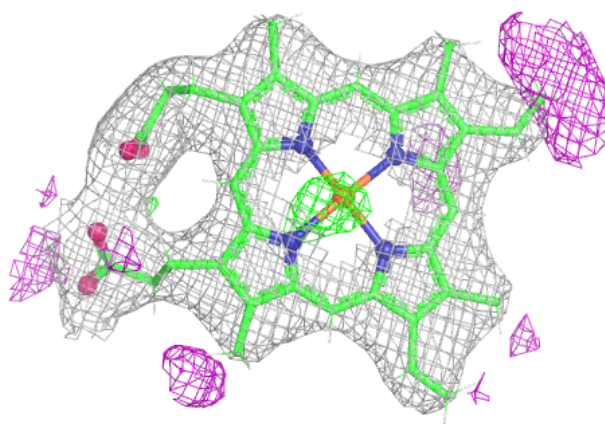
Electron density around HEM C 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



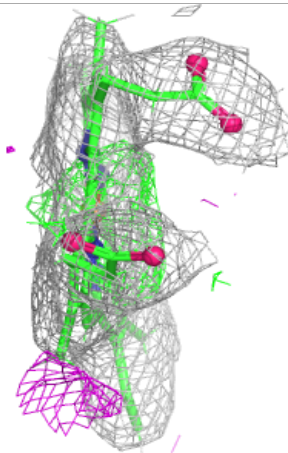
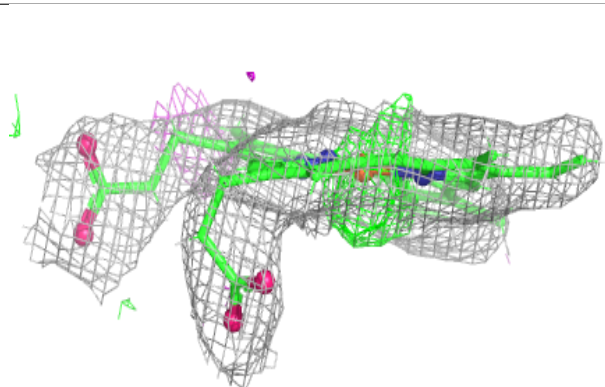
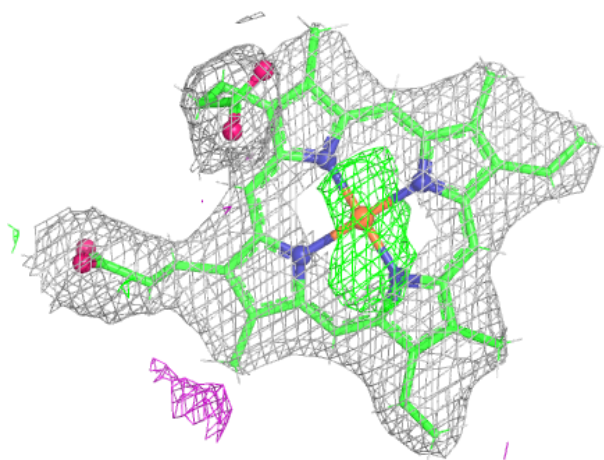
Electron density around HEM A 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 302:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.